IN THE CLAIMS:

The text of all pending claims, (including withdrawn claims) is set forth below. Cancelled and not entered claims are indicated with claim number and status only. The claims as listed below show added text with <u>underlining</u> and deleted text with ~~strikethrough~~. The status of each claim is indicated with one of (original), (currently amended), (cancelled), (withdrawn), (new), (previously presented), or (not entered).

1. (currently amended) A method for supporting a user in predicting ~~a site where a target gene on a genome is expressed~~<u>a gene expression site</u>, the<u> gene expression</u> site being one of a cell, a tissue<u>,</u> and an organ, said method comprising:

calculating a ~~first~~ distance between ~~the target gene and~~ a first gene ~~on the genome and a second distance between the target gene and a second gene on the genome, where the first distance is smaller than the second distance;~~

~~extracting, from a database, a first site where the first gene is expressed and a second site where the second gene is expressed; and~~<u>and each of a plurality of second genes on a genome sequence, wherein the first gene is an unknown gene whose gene expression site is unknown, while the second genes are known genes whose expression sites are known;</u>

<u>determining the gene expression site of the first gene based on the distance, wherein the determining includes determining as the gene expression site of the first gene, a gene expression site of at least one of the second genes that has a predetermined distance relation with the first gene, the predetermined distance relation being determined based on a sensitivity and a specificity; and</u>

outputting~~, as a list in which the first site is listed above the second site, a plurality of sites where the target gene is likely to be expressed~~ <u>the gene expression site of the first gene determined by the determining</u>.

2. (previously presented) The method according to claim 1, wherein both the first distance and the second distance are smaller than a predetermined threshold.

3. (previously presented) The method according to claim 1, wherein the first distance is between a start position of the target gene and a start position of the first gene, and the second distance is between the start position of the target gene and a start position of the second gene.

4. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the end position of the first gene and the end position of the second gene on the genome sequence.

5. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the start position of the first gene and the end position of the second gene on the genome sequence.

6. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the end position of the first gene and the start position of the second gene on the genome sequence.

7. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between first and second positions, the first position being between the start and end positions of the first gene on the genome sequence, and the second position being between the start and end positions of the second gene on the genome sequence.

8. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between a position between the start and end positions of the first gene and the start position of the second gene on the genome sequence.

9. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between a position between the start and end positions of the first gene and the end position of the second gene on the genome sequence.

10. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the start position of the first gene and a position between the start and end positions of the second gene on the genome sequence.

11. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the end position of the first gene and a position between the start and end positions of the second gene on the genome sequence.

12-24. (cancelled)

25. (currently amended) A computer program product including computer executable instructions supporting a user in predicting ~~a~~ a gene expression site, ~~a site where a target gene on a genome is expressed~~, the gene expression site being one of a cell, a tissue and an organ, and wherein the instructions, when executed by the computer, cause the computer to perform a method comprising:

calculating a ~~first~~ distance between ~~the target gene and~~ a first gene ~~on the genome and a second distance between the target gene and a second gene on the genome, where the first distance is smaller than the second distance;~~ and each of a plurality of second genes on a genome sequence, wherein the first gene is an unknown gene whose gene expression site is unknown, while the second genes are known genes whose expression sites are known;

determining the gene expression site of the first gene based on the distance, wherein the determining includes determining as the gene expression site of the first gene, a gene expression site of at least one of the second genes that has a predetermined distance relation with the first gene, the predetermined distance relation being determined based on a sensitivity and a specificity; and

~~extracting, from a database, a first site where the first gene is expressed and a second site where the second gene is expressed; and~~

outputting, ~~as a list in which the first site is listed above the second site, a plurality of sites where the target gene is likely to be expressed~~ the gene expression site of the first gene determined by the determining.

26. (previously presented) The computer program product according to claim 25, wherein both the first distance and the second distance are smaller than a predetermined threshold.

27. (cancelled)

28. (currently amended) An apparatus for supporting a user in predicting ~~a site where a target gene on a genome is expressed~~ a gene expression site, where the site is one of a cell, a tissue and an organ, said apparatus comprising:

a calculating unit that calculates a ~~first~~ distance between ~~the target gene and a first gene on the genome and a second distance between the target gene and a second gene on the genome, where the first distance is smaller than the second distance;~~ and each of a plurality of

4

second genes on a genome sequence, wherein the first gene is an unknown gene whose gene expression site is unknown, while the second genes are known genes whose expression sites are known;

~~an extracting unit that extracts, from a database, a first site where the first gene is expressed and a second site where the second gene is expressed; and~~

a determination unit that determines the gene expression site of the first gene based on the distance, wherein the determining includes determining as the gene expression site of the first gene, a gene expression site of at least one of the second genes that has a predetermined distance relation with the first gene, the predetermined distance relation being determined based on a sensitivity and a specificity; and

an output unit that outputs the gene expression site of the first gene determined by the determination unit~~, as a list in which the first site is listed above the second site, a plurality of sites where the target gene is likely to be expressed.~~

29. (previously presented) The apparatus according to claim 28, wherein both the first distance and the second distance are smaller than a predetermined threshold.

30. (cancelled)

31. (previously presented) The method according to claim 1, wherein when the first site and the second site are identical, the second site is deleted from the list before being output.

32. (cancelled)

33. (new) The method according to claim 1, wherein

the sensitivity is a ratio of expression sites predicted to expression sites previously determined that it is where the unknown gene expresses by other method, and

the specificity is a ratio of expression sites not predicted to expression sites previously determined that it is where the unknown gene never expresses by the other method.

34. (new) A method of supporting a user in determining a gene expression site, comprising:

calculating the distance of an unknown gene having an unknown gene expression site from each of a plurality of known genes on a genome sequence having known gene expression

sites; and

       outputting a gene expression site of the unknown gene, the gene expression site determined by measuring the distance between a gene expression site of at least one of the known genes and the unknown gene based on based on a sensitivity and a specificity.